

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Frame	Sign.
***** 2 standard deviations above mean *****					
1. US-08-394-189b-2	Sequence 2, Application 0	503	493	493	2.49
1. US-09-577-897-19 (1-503)					
US-08-394-189b-2					
Initial Score	=	493	Optimized Score	=	493
Residue Identity	=	98%	Matches	=	493
Gaps	=	0	Conservative Substitutions	=	10
X	10	20	30	40	50
MMHODRRSLLENINIMFSSHLKVDLEILLEVLAKQVLSNDGMDHNSCGTYREKREITKAVORGDVADF					
MMHODRRSLLENINIMFSSHLKVDLEILLEVLAKQVLSNDGMDHNSCGTYREKREITKAVORGDVADF					
X	10	20	30	40	50
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
X	10	20	30	40	50
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
X	10	20	30	40	50
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
X	10	20	30	40	50
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
X	10	20	30	40	50
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
X	10	20	30	40	50
YDALRSTGHEGLAEVLPLARSVDSNNAVEFECPCSPASHRRSRALSPAGTSPTRYHRDVSVSSPSTYOD					
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X	10	20	30	40	50
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